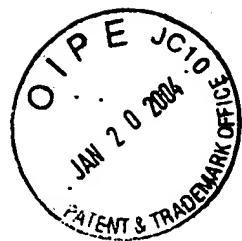




MULTIPLE ALIGNMENT:
SPI MULTIPLE ALIGNMENT:
CA
SPI
CA SPKinaseinHSDA59H18
SPI CAB62977
CA
SPI SPKinaseinHSDA59H18
CA CAB62977
SPI
CA SPKinaseinHSDA59H18
CA CAB62977
SPI
CA SPKinaseinHSDA59H18
SPI CAB62977
CA
SPKinaseinHSDA59H18
CAB62977
SPKinaseinHSDA59H18
CAB62977
SPKinaseinHSDA59H18
CAB62977
SPKinaseinHSDA59H18
CAB62977

MEKPYAFTHVCVKRARRHRKWAQVTFWCPEEQICHILWLQTLREMLEKLTSPKHLLVFI
-----PKHLLVFI
NPFGGKGQGRKRIYERKVAPLFTLASITTDIIGNKFYNNVEVITEHANQAKETLYEINID
NPFGGKGQGRKRIYERKVAPLFTLASITTDIIGNKFYNNVEVITEHANQAKETLYEINID
KYDGIIVCVGGDGMFSEVLHGLIGRTORSAGVDQNHPRAVLVPSSLRIGIIPAGSTDVCVY
KYDGIIVCVGGDGMFSEVLHGLIGRTORSAGVDQNHPRAVLVPSSLRIGIIPAGSTDVCVY
STVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLGFGFYGDI IKDSEKKRWL
STVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLGFGFYGDI IKDSEKKRWL
GLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPPDRKPCRCAGCFVCRQSKQQLLEEQK
GLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPPDRKPCRCAGCFVCRQSKQQLLEEQK
KALYGLEAAEDVEEWQVCGKFLA INATNMSCACRRSPRGLSPAHLGDGSSDLILIRKC
KALYGLEAAEDVEEWQVCGKFLA INATNMSCACRRSPRGLSPAHLGDGSSDLILIRKC
SRFNFLRFLIRHTNQDDQDFTFVEVYRVKKQFTSKHMEDESDLKEGGKRFGHICSS
SRFNFLRFLIRHTNQDDQ-----
HPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS

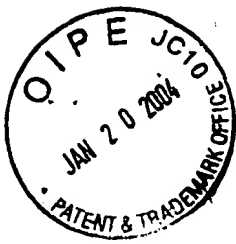
FIG. 1



MULTIPLE ALIGNMENT:

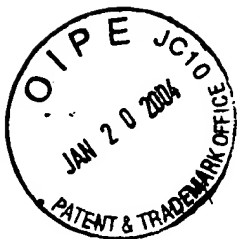
52180312	-----
A1237625	-----
SPKinaseinHSDA59H18	PKHLLVFINPFGGKGQGGKRIYERKVAPLFTLASITTDIIGNKFYVYVEVITEHANQAKE
52180312	-----
A1237625	-----
SPKinaseinHSDA59H18	TLYEINIDKYDGI VCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA
52180312	-----
A1237625	-----
SPKinaseinHSDA59H18	GSTDCVCYSTVGTSDAETSA LHI VVGDSLAMDVSSVHHNSTLLRYSVSLG YGYGDI I K
52180312	-----
A1237625	-----
SPKinaseinHSDA59H18	DSEKKRWLGLARYDFSG LKTF LSHHCYEGTVSFLPAQHTVGS PRDRKPC RAGCFVCRQSK
52180312	-----
A1237625	-----
SPKinaseinHSDA59H18	QQL EEEQKKALYGLEAAEDVEEWQVCGKFLA I N A I N N M S C A C R R S P R G L S P A A H L G D G S S
52180312	-----
A1237625	-----
SPKinaseinHSDA59H18	DL I L I R K C S R E N F L R L I R H T N Q D Q D F T F V E V Y R V K K F Q T S K H V E D D N D L K E I L E K Q
52180312	-----
A1237625	-----
SPKinaseinHSDA59H18	KFGK I C K D R P S C I T S A S R S S W N C D G E V M H S P A T E V R V H C Q L V R L F A R G I E E S
52180312	-----
A1237625	-----
SPKinaseinHSDA59H18	R E F G H I C S S H P S C C C I V S N S S W N C D G E V L H S P A T E V R V H C Q L V R L F A R G I E E N P K P D S H S

FIG. 2



C5

coorected_human_sphingosine AF068748_EXT-2	AAALRTVRCPLATLTVRVGF-----KTP----- ASLRITVQCCLAYLVEIVAS-----KRP----- IQKKKYPCEIYVKYAAKSKNELKNHYLEHKNKGSLEFQHTMNKDNEDCDNYYENEYET IQKKKYPCEVFKYAAKSKKELKVHFLNKDK-----NKGCLTFE-PNPSPN EQKPDWKCSTIEMDVSSDRTEIKHMYE-----KSK----- CNLRVYKCPITVRYPKPKGFHPSSNVFSVEK-----TTQQRID----- LSHHCYEGTVSFLPAQHTVGSFRD-----RKP-----CRAGCFVCR-----
SPkinaseinHSDA59H18	-----ASPVVVQQ-----GFVDAHLVPLTFEQ-MPSHWQVWP-----D -----ASTLVQK-----GHVDTHLVPLTFEP-MPSHWITVWP-----E ENEDEDADADEDSHLATSRDLADSSADQ-IKEEDFKIKYPLDEG-IPSDWERLDPNIS SSPDLLSKNNINNSTKDELSPNFLN-----EDNFKLKYVWTEP-MPRDWEKMDSELT -----N-----LAPMSES-----SDSKTVSTSP-----SHLLTFE-----I -DSKVKTNGSVSDSEETMETKFN-----WTIPDSDDETAVG-SSDLEETVW-----IE QSKQQLSEEQKALYGLEAAEDVEEWQVCGKFLATNATNMNSCACRRSERRGLSPAAGLGD
coorected_human_sphingosine AF068748_EXT-2	EDFVLIALLSHLSLASEMFAAPMGRCAAGMWHILFYVRAQVSRAMLLRIFLAMEKGRHMEY QDFVLVLVLLHHLSSSELFAAPMGRCEAGMWHILFYVRAQVSRAMLLRIFLAMEKGRHMEY NNLGLFYTGKMPYVADTKFFPAALPSDCTMDWITLARTSLTRMAPILGLDKC--SHV DNLTIFYTGKMPYVADTKFFPAALPADGTIDVITLARIPVTRMTFHLSDDKC--SHV NDLSLFCAGLLPYIAPDAKMFPAASNDGLIDVLYSKQKPKSLSMFTQDNG--GFY DNFVNITYAVTLSHIADGPFAPSAKLEBNRIHLSYLLWKDIGTRVNIKYLLAIEGETH GSSDLJLIRKCSRNFRLIRHTNQDQDFTFVEVYRVKQFQTSKIMEDDESDLKEG
SPkinaseinHSDA59H18	ECPLYLVVVPVVAFRLEPKDGK-----VFAVDGELMVSEAVQGOVHBNYFVMVSGCVEPPPS DCPLYLVVVPVVAFRLEPRSOR-----VFSVDGELMVCEAVQGOVHBNYLMVCGSRDAPSG LQPEVHLSKLLAYKHIPKICNG-----LFSVDGELKFPLEPLQVEIMPRIECKTLR----- LEPEVHLSKLLAYKHIPKIVESC-----LFSVDGELKFPLEPLQVEIMPRIECKTLR----- YSKHINYYKVRSEFETLVNTEKRYHEALDGESEYPLEPPEECRMAEKLTLSLSP-----V DLPEVHLSKLLAYKHIPKIVESC-----HVLIDGELVDKTEVASTKNHISVFSSTA----- GKKRFCHICSSHPSCCCVMSNS-----SNVDGELVHSPATEVVRTHQCVRLFAR-----
coorected_human_sphingosine AF068748_EXT-2	WKQQMPPPPPEPPL RDSRRGPPPEEP -NGRYVDTDFDSM -NGRYVDTDFESM AGFQLLDI----- ----- -GIENPKPDSHS
SPkinaseinHSDA59H18	



PHYLIP - PROTEIN DISTANCE ANALYSIS

SEQUENCES ANALYZED:

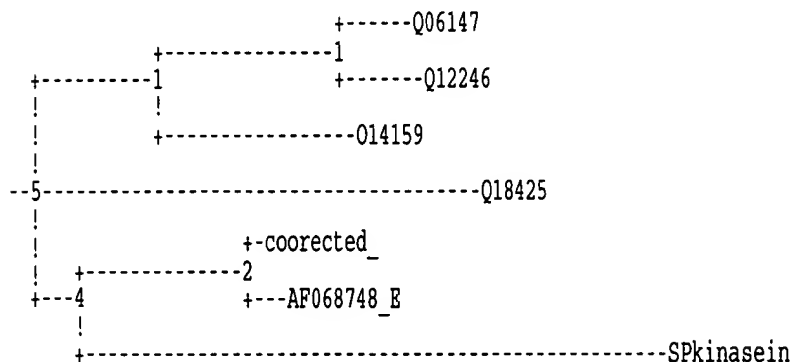
1. SPkinaseinHSDA59H18
2. Q18425
3. O14159
4. Q06147
5. Q12246
6. coorrected_human_sphingosine
7. AF068748_EXT-2

7 POPULATIONS

NEIGHBOR-JOINING/UPGMA METHOD VERSION 3.572c

NEIGHBOR-JOINING METHOD

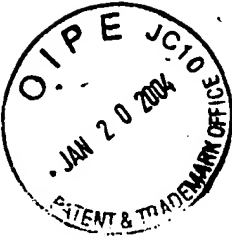
NEIGHBOR BRANCH LENGTHS ALLOWED



REMEMBER: THIS IS AN UNROOTED TREE!

BETWEEN	AND	LENGTH
5	3	1.09970
3	1	1.59865
1	Q06147	0.79847
1	Q12246	1.02742
3	O14159	1.74537
5	Q18425	4.00995
5	4	0.43259
4	2	1.44382
2	coorrected_	0.24774
2	AF068748_E	0.37392
4	SPkinasein	5.26443

FIG. 4



MULTIPLE ALIGNMENT:

80432911 SPkinaseinHSDA59H18	ACAPGADACSVPVSEI.IAVEETDVHGKHQSGKWKQMEKPYAFTVHCVKRARRHRWKWAQ -----MEKPYAFTVHCVKRARRHRWKWAQ
80432911 SPkinaseinHSDA59H18	VTFWCPPEEQ.LCHLWLQTLREMLEKLT.SRP.KHLLVFINPFGGKGQKRIYERKVAPLETLA VTFWCPPEEQ.LCHLWLQTLREMLEKLT.SRP.KHLLVFINPFGGKGQKRIYERKVAPLETLA
80432911 SPkinaseinHSDA59H18	SITTTDII-----VTEHANOAKETLYEINIKVDYDGI.VCVGGDGMFSEVLHGLIGR SITTTDII.GNKFVYNYVEVITTEHANOAKETLYEINIKVDYDGI.VCVGGDGMFSEVLHGLIGR
80432911 SPkinaseinHSDA59H18	TORSAGVDONHPR----- TORSAGVDONHPRAVLVPSSLRIGI.I.PAGSTDCVCYSTVGTSDAETSALH.I.VWGD.SLAMD
80432911 SPkinaseinHSDA59H18	VSSVHHNSTLLRYSVSLGYGYGDI.IKDSEKKRWLGLARYDFSG.LKTF.LSHHCYEGTVS -----
80432911 SPkinaseinHSDA59H18	FLIPAQHTVGSPRDRKPCRAGCFV.CROSKQQL.EEEQKKALYGLEAAEDVEEWQV.VCGKFLA -----
80432911 SPkinaseinHSDA59H18	INATNMSCACRRSPRGLSPAHLGDGSSDL.I.IRKCSR.FNFLRFLIRHTNQDQDFDFTFV -----
80432911 SPkinaseinHSDA59H18	EVYRVKKFQETSKHMEDESD.I.KEGGKRF.GHICSSHPSCCCTVSNSSWNCDGEVLHSPA -----
80432911 SPkinaseinHSDA59H18	IEVRVHCQLVRLFARGIEENPKPDSHS -----

FIG. 5